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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/698,903B

DATE: 10/01/2001

TIME: 13:39:15

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\10012001\I698903B.raw

3 <110> APPLICANT: Weston, et al.
 5 <120> TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING SAME
 7 <130> FILE REFERENCE: 514412-2020.1
 9 <140> CURRENT APPLICATION NUMBER: 09/698,903B
 10 <141> CURRENT FILING DATE: 2000-10-27
 12 <150> PRIOR APPLICATION NUMBER: 09/430,437
 13 <151> PRIOR FILING DATE: 1999-10-29
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: Patentin version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5865
 21 <212> TYPE: DNA
 C--> 22 <213> ORGANISM: Artifical Sequence ✓
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (1)..(5865)
 27 <223> OTHER INFORMATION: DNA sequence of regions comprised between the T-DNA border

repeat

28 s of plasmid pTC0113

31 <400> SEQUENCE: 1

| | | | | | | | |
|----|-------------|-------------|-------------|-------------|-------------|-------------|------|
| 32 | aattacaacg | gtatataatcc | tgccagtaact | cggccgtcga | actcggccgt | cgagtagatg | 60 |
| 34 | gtcgataaga | aaaggcaatt | tgttagatgtt | aattcccac | ttgaaagaaa | taatagttaa | 120 |
| 36 | atattttattg | ataaaaataac | aagtcaaggt | ttatagtcca | agcaaaaaca | taaattttatt | 180 |
| 38 | gatcaagtt | taaattcaga | aatatttcaa | taactgatta | tatcagctgg | tacattgccg | 240 |
| 40 | tagatgaaag | actgagtgcg | atattatgt | taatacataa | attgtatgata | tagctagctt | 300 |
| 42 | agctcatcg | gggatcttag | aacgcgtgat | ctcagatctc | ggtgacgggc | aggaccggac | 360 |
| 44 | ggggcggta | cggcaggctg | aagtccagct | gccagaaacc | cacgtcatgc | cagttcccg | 420 |
| 46 | gcttgaagcc | ggccgcggc | agcatgccc | ggggggcata | tccgagcgc | tcgtgcatgc | 480 |
| 48 | gcacgctcg | gtcgccccgc | agcccgatga | cagcaccac | gctcttgaag | ccctgtgcct | 540 |
| 50 | ccagggactt | cagcagggtgg | gtgttagagcg | tggagccag | tccctccgc | tggggcggg | 600 |
| 52 | gggagacgta | cacggtcac | tccggcgtcc | agtcgttaggc | tttcgcgtgc | ttccaggggc | 660 |
| 54 | cccgcttaggc | gatgccggcg | acctcgccgt | ccacctcgcc | gacgagccag | ggatacgct | 720 |
| 56 | cccgcagacg | gacgaggctcg | tccgtccact | cctcggttc | ctgcggctcg | gtacggaagt | 780 |
| 58 | tgaccgtgct | tgtctcgat | tagtgggtga | cgatggtgca | gaccgcggc | atgtccgcct | 840 |
| 60 | cggggcacg | gcggatgtcg | gccggggcgtc | gttctgggtc | cattgttctt | ctttactctt | 900 |
| 62 | tgttgtgactg | aggttggtc | tagtgcctt | gtcatctata | tataatgata | acaacaatga | 960 |
| 64 | gaacaagctt | tggagtgatc | ggagggtcta | ggatacatga | gattcaagtg | gactaggatc | 1020 |
| 66 | tacaccgttg | gattttgagt | gtggatatgt | gtgaggtta | tttacttgg | taacggccac | 1080 |
| 68 | aaaggcctaa | ggagagggtgt | tgagaccctt | atcggttga | accgctggaa | taatgccacg | 1140 |
| 70 | tggaaagataa | ttccatgaat | cttatcgta | tctatgatg | aaattgtgt | atggggagt | 1200 |
| 72 | ggtgcttgct | cattttactt | gcctgggtgg | cttggccctt | tccttatgg | gaatttat | 1260 |
| 74 | tttacttact | atagagctt | catacctttt | ttttaccttg | gattttagtta | atataataatg | 1320 |
| 76 | gtatgattca | tgaataaaaa | tggaaattt | ttgaatttgt | actgctaaat | gcataagatt | 1380 |
| 78 | aggtgaaact | gtgaaatata | tattttttc | atttaaaagc | aaaatttgc | ttttactaga | 1440 |
| 80 | attataaata | tagaaaaata | tataacattc | aaataaaaat | gaaaataaga | actttcaaaa | 1500 |
| 82 | aacagaacta | tgttaatgt | gtaaagatta | gtcgacatc | aagtcatctg | ttacaatatg | 1560 |
| 84 | ttacaacaag | tcataagccc | aacaaagtt | gcacgtctaa | ataaaactaaa | gagtccacga | 1620 |
| 86 | aaatattaca | aatcataa | ccaaacaaagt | tattgatcaa | aaaaaaaaaa | cgcccaacaa | 1680 |

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| 88 | agctaaacaa agtccaaaaa aaacttctca agtctccatc ttcccttatg aacattgaaa | 1740 |
| 90 | actataca caaacaagtca gataaatctc tttctggcc tgtctccca acctcctaca | 1800 |
| 92 | tcacttccct atcgattga atgtttact tgtaccttt ccgttgcata gatattgata | 1860 |
| 94 | gtatgttgt gaaaactaat agggttaaca atcgaagtca tggatatagg atttggcca | 1920 |
| 96 | agatttccg agagcttct agtagaaagc ccatcaccag aaatttacta gtaaaataaa | 1980 |
| 98 | tcaccaatta gtttcttat tatgtgccaa attcaatata attatagagg atatttcaaa | 2040 |
| 100 | tgaaaacgta tgaatgttat tagtaaatgg tcaggtaaaga cattaaaaaa atcc tacg | 2100 |
| 102 | agatattcaa cttaaaaat tcgatcagt tggaaattgt aaaaaatttgg gatctacta | 2160 |
| 104 | tatataatata atgcatttaca acacttggat tttttttgg aggctgaaat tttttaatcta | 2220 |
| 106 | cataatttgg ttggccatgc accaactcat tgtttagt aatacttga ttttgtaaaa | 2280 |
| 108 | tatatgtgtt cgtgtatatt tggataagaa ttctttgac catatacacaa cacacatata | 2340 |
| 110 | tatataatata tatatattat atatcatgca cttaatttgg aaaaataat atatataat | 2400 |
| 112 | atagtgcatt ttttctaaca accatataat ttcgcatttga tctgcaaaaa tactgctaga | 2460 |
| 114 | gtaatgaaaa atataatcta ttgctgaaat tatctcagat gttaaagatt tcttaaagta | 2520 |
| 116 | aattcttca aatttttagct aaaagtcttga taataactaa agaataatac acaatctcga | 2580 |
| 118 | ccacggaaaaaaa acacacata ataaatttga atttcgaccg cggtacccgg aattc gagct | 2640 |
| 120 | cggtacccgg ggatcttccc gatctgat ttcgcatttgc accgcgcgcg ataaatttata | 2700 |
| 122 | ctagttgcg cgctatattt tgtttctat cgcgtattaa atgtataattt gcgggactct | 2760 |
| 124 | aatcataaaaa acccatctca taaataacgt catgcatttac atgttaattt ttacatgctt | 2820 |
| 126 | aacgttaattt aacagaaattt atatgataat catcgcaaga cccgcacag gattcaatct | 2880 |
| 128 | taagaaaaattt tattgccccaa tgtttgcacg atctgcatttgc gatcctctag agccggaaag | 2940 |
| 130 | tgaaaatttgc acgtcagagt ttgaaagaaaa atttattaca cactttatgt aaagctgaaa | 3000 |
| 132 | aaaacggcct ccgcaggaaag ccgtttttt cgttatctga ttttgcataa ggtctgataa | 3060 |
| 134 | tggccgtt ttttgcataa cagccagtcg cttgagtaaa gaatccggc tgaatttctg | 3120 |
| 136 | aagcctgatg tatagtttaat atccgcattca cgcatttgc gtcgcctttt gcccgggagtt | 3180 |
| 138 | ttgccttccc tgtttgcataa gatgtctccg ccgcatttgc tccccggagc gacgtctgca | 3240 |
| 140 | aggcccctt ttgcattccac ccagccgagg gcttgcatttgc ctgattttgt aatgtat | 3300 |
| 142 | ttaggtatct tatgatatgt ctgcatttttttgc tccgcaccc cgtcaacgt gttgataacc | 3360 |
| 144 | ggtaccatgg tagctatattt cttaagtaa aaactttgtt tgagtgtatg atgttgcact | 3420 |
| 146 | gttacacttgc caccacaaagg gcatatataatg agcacaagac atacacaaca acttgc | 3480 |
| 148 | ctaacttttgc ttggcatttcgatcggaaaaa tggggatgg caggctatc tgagggttac | 3540 |
| 150 | attaagggtt catgtattaa ttgttgcataa acatggactt agtgcgttggaaaatgacca | 3600 |
| 152 | aaattttgtt tcaccctgtat ttgcatttgcataa gaaatttacat tatgtatgt tgctagagaa | 3660 |
| 154 | gtatgttttgc ttagtccatc caccacatc atgcatttgc gcttttagt tgattcaaaa | 3720 |
| 156 | actgatattaa ttgcatttgcataa taaatgttgcataa tacttgcatttgc ctatgtcgat ttaatttgc | 3780 |
| 158 | taggtatctt atatttgcataa ataaaaatc atgttgcataa catcttgcataa aatgtgacaa | 3840 |
| 160 | gtcaatttgc ctttgcatttgcataa ttgcatttgcataa ttcaatctgt taatgcataat tattcatttgc | 3900 |
| 162 | tacttagtca gatatttgcataa ttgttgcataa aatgttgcataa gtttgcataa ccggatgttgc | 3960 |
| 164 | acaaagtccatc atatccatca aacttgcatttgcataa gtttgcataa aatgttgcataa ccggatgttgc | 4020 |
| 166 | ttaaaaatttttgcataa aatgttgcataa gatatttgcataa ttgttgcataa aatgttgcataa ccggatgttgc | 4080 |
| 168 | acagattgtt acatggaaaaa caaaaatgtcc tctgtatgttgcataa gtttgcataa aatgttgcataa ccggatgttgc | 4140 |
| 170 | tctatcgatc gatatttgcataa aatgttgcataa gtttgcataa aatgttgcataa ccggatgttgc | 4200 |
| 172 | gtctaaatttgcataa atgttgcatttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4260 |
| 174 | ttttttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4320 |
| 176 | atatttgcataa ttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4380 |
| 178 | aatgttgcataa ttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4440 |
| 180 | aaaatgttgcataa ttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4500 |
| 182 | aaaatgttgcataa ttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4560 |
| 184 | acatggaaaaa aatgttgcataa ttttgcataa aatgttgcataa ttttgcataa aatgttgcataa ccggatgttgc | 4620 |

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| | |
|--|------|
| 186 gcaacaagta tcaatacata tgatttacac cgtccaaacac gaaattcgta aatatttaat | 4680 |
| 188 ataataaaaga attaatccaa atagcctccc accctataac ttaaaactaaa aataaccagc | 4740 |
| 190 gaatgtatat tatatgcata atttatataat taaatgtgt aataatgtgt aataatgt | 4800 |
| 192 ataatctatg tatatggta gaaaaagtaa acaattaata tagccggta tttgtgtaaa | 4860 |
| 194 aatccctaataatcgca cggatccccg ggaattccgg ggaagcttag atccatgcag | 4920 |
| 196 atctgatcat gagcggagaa ttaaggaggta cacgttatga ccccccgcga tgacgcggga | 4980 |
| 198 caagccgttt tacgtttgga actgacagaa ccgcaacatg tgaaggagcc actcagccgc | 5040 |
| 200 gggtttctgg agttaatga gctaagcaca tacgtcagaa accattattg cgcgttcaa | 5100 |
| 202 agtcgcctaa ggtcaactac agctagcaaa tatttcttgta caaaaatgt ctactgacgt | 5160 |
| 204 tccataaaatt cccctcggtt tccaatttga gtctcatatt cactctcaat ccaaaccatg | 5220 |
| 206 aaaaaggcag tcattaacgg ggaacaatc aagaatgtatca ggcacccca ccagacattg | 5280 |
| 208 aaaaaggagc ttgccttcc ggaataactac ggtgaaaacc tggacgttt atgggattgt | 5340 |
| 210 ctgaccggat gggggagta cccgctcggtt ttggatggta ggcagttga acaaagcaag | 5400 |
| 212 cagctgactg aaaatggcgc cggaggtgtg cttcagggtt tccgtgaagc gaaagcggaa | 5460 |
| 214 ggctgcgacatc tcaccatcat actttcttaa tacgtatcaat gggagatgaa caatatggaa | 5520 |
| 216 acacaaaccc gcaagcttgg ttagaggat ccccccgtatg gctaagctag ctatatcatc | 5580 |
| 218 aatttatgtt ttacacataa tatcgactc agtcttcat ctacggcaat gtaccagctg | 5640 |
| 220 atataatcg ttatttggaaat atttctgtat ttaaacttgc atcaataat ttatgtttt | 5700 |
| 222 gcttggacta taataacctga cttgttattt tatcaataaa tatttaact atatttcttt | 5760 |
| 224 caagatggga attaacatct acaaattgcc ttttcttgc gaccatgtac atcgagctct | 5820 |
| 226 ccccgatct gcatggagcc atttacaatt gaatataatcc tgccg | 5865 |
| 229 <210> SEQ ID NO: 2 | |
| 230 <211> LENGTH: 21 | |
| 231 <212> TYPE: DNA | |
| 232 <213> ORGANISM: Artificial Sequence | |
| 234 <220> FEATURE: | |
| 235 <221> NAME/KEY: misc_feature | |
| 236 <222> LOCATION: (1)..(21) | |
| 237 <223> OTHER INFORMATION: primer MDB355 | |
| 240 <400> SEQUENCE: 2 | |
| 241 gtaacataga tgacacccgcg c | 21 |
| 244 <210> SEQ ID NO: 3 | |
| 245 <211> LENGTH: 21 | |
| 246 <212> TYPE: DNA | |
| 247 <213> ORGANISM: Artificial Sequence | |
| 249 <220> FEATURE: | |
| 250 <221> NAME/KEY: misc_feature | |
| 251 <222> LOCATION: (1)..(21) | |
| 252 <223> OTHER INFORMATION: primer MLD008 | |
| 255 <400> SEQUENCE: 3 | |
| 256 atagggtggg aggctatttg g | 21 |
| 259 <210> SEQ ID NO: 4 | |
| 260 <211> LENGTH: 15 | |
| 261 <212> TYPE: DNA | |
| 262 <213> ORGANISM: Artificial Sequence | |
| 264 <220> FEATURE: | |
| 265 <221> NAME/KEY: misc_feature | |
| 266 <222> LOCATION: (1)..(15) | |
| 267 <223> OTHER INFORMATION: primer MDB285 | |

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270 <220> FEATURE:
271 <221> NAME/KEY: variation
272 <222> LOCATION: (6)..(6)
273 <223> OTHER INFORMATION: "s" can be either g or c
276 <220> FEATURE:
277 <221> NAME/KEY: variation
278 <222> LOCATION: (1)..(1)
279 <223> OTHER INFORMATION: "n" can be any nucleotide a, c, t or g
282 <220> FEATURE:
283 <221> NAME/KEY: variation
284 <222> LOCATION: (8)..(8)
285 <223> OTHER INFORMATION: "w" can be either a or t(u)
288 <220> FEATURE:
289 <221> NAME/KEY: variation
290 <222> LOCATION: (12)..(12)
291 <223> OTHER INFORMATION: "w" can be either a or t(u)
294 <220> FEATURE:
295 <221> NAME/KEY: variation
296 <222> LOCATION: (10)..(10)
297 <223> OTHER INFORMATION: "s" can be either g or c
300 <400> SEQUENCE: 4
W--> 301 ntcgastwts gwgtt 15
304 <210> SEQ ID NO: 5
305 <211> LENGTH: 25
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <222> LOCATION: (1)..(25)
312 <223> OTHER INFORMATION: primer MDB251
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316 ggatcccccg atgagctaag ctac 25
319 <210> SEQ ID NO: 6
320 <211> LENGTH: 22
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <221> NAME/KEY: misc_feature
326 <222> LOCATION: (1)..(22)
327 <223> OTHER INFORMATION: primer MDB193
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331 tcatactacgg caatgtacca gc 22
334 <210> SEQ ID NO: 7
335 <211> LENGTH: 20
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337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <221> NAME/KEY: misc_feature
341 <222> LOCATION: (1)..(20)

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342 <223> OTHER INFORMATION: primer MDB258
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 346 ctacggcaat gtaccagctg 20
 349 <210> SEQ ID NO: 8
 350 <211> LENGTH: 415
 351 <212> TYPE: DNA
 352 <213> ORGANISM: Artificial Sequence
 354 <220> FEATURE:
 355 <221> NAME/KEY: misc_feature
 356 <222> LOCATION: (1)..(415)
 357 <223> OTHER INFORMATION: right (5') border flanking region of elite event MS-B2
 360 <400> SEQUENCE: 8
 361 gtcgagttt gtttttttt tgactcttca ccattacata ttgaaactct 60
 363 tacggatgag aacaactcac aagcattaat catgttcata taaaatataatg tacattatac 120
 365 gatatataac acgtatacaa atatgttagcga agaaatccat gtaaaaggcagc agggggcacc 180
 367 atggtttcaa gtattatata attataatata taattatgtt aggatgtaca tggccgataa 240
 369 gaaaaggcaa tttgttagatg ttaattccca tcttggaaaga aatatagttt aaatatttat 300
 371 tgataaaaata acaagtctagg tattatagtc caagaaaaa cataaaattta ttgtatgc 360
 373 tttaaaattca gaaatatttc aataactgtat tataatcgat ggtacattgc cgtag 415
 376 <210> SEQ ID NO: 9
 377 <211> LENGTH: 24
 378 <212> TYPE: DNA
 379 <213> ORGANISM: Artificial Sequence
 381 <220> FEATURE:
 382 <221> NAME/KEY: misc_feature
 383 <222> LOCATION: (1)..(24)
 384 <223> OTHER INFORMATION: primer MDB8
 387 <400> SEQUENCE: 9
 388 tcagaagttt cagcgcaccc cacc 24
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 392 <211> LENGTH: 416
 393 <212> TYPE: DNA
 394 <213> ORGANISM: Artificial Sequence
 396 <220> FEATURE:
 397 <221> NAME/KEY: misc_feature
 398 <222> LOCATION: (1)..(416)
 399 <223> OTHER INFORMATION: left (3') border flanking region of the elite event MS-B2
 402 <400> SEQUENCE: 10
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 405 atcaataaaaw ttatgtttt gcttggacta taatacctga cttgttattt tatcaataaaa 120
 407 tatttaaaact atatttcttt caagatggga attaacatct acaaatttgc ttttcttatac 180
 409 gaccatgtac atcctaccat aattataatt ataattatata aataactgaaa ccatggtgcc 240
 411 ccctgctgtt ttacatggat ttctccgcta ctatttgtat acgtgtatata ataccgtata 300
 413 atgtacatata atttatatac acatgattaa tgcttgcgat ttgttctcat ccgtaaagat 360
 415 ttcaaatatgt aatggtgaag agtcaaaacc caaaatcatg aacacccaaa ctcgat 416
 418 <210> SEQ ID NO: 11
 419 <211> LENGTH: 23
 420 <212> TYPE: DNA
 421 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY
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L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4